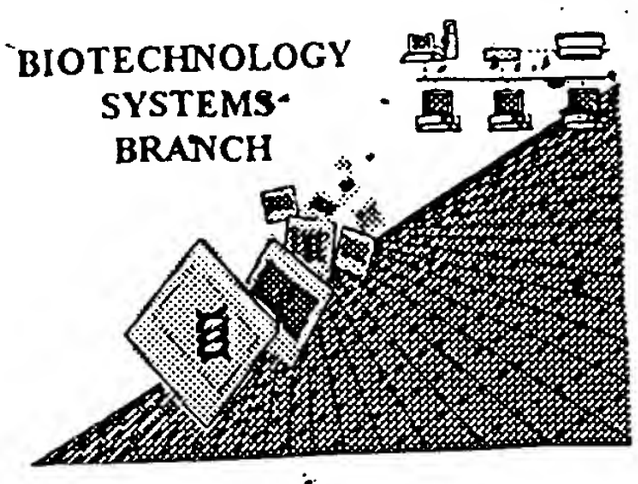

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: US 09 840 243A

Source: OIPE

Date Processed by STIC: 10/29/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/940243A

ERROR DETECTED	SUGGESTED CORRECTION
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P	
1____Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2____Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3____Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4____Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5____Variable Length.	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6____PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7____Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8____Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequen <210> sequence id number <400> sequence id number 000
9__✓__Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
10____Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence
11____Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (See. 1.823 of Sequence Rules)
12____PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13____Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represe any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING DATE: 10/29/2001
PATENT APPLICATION: **US/09/840,243A** TIME: 13:29:31

Input Set : **A:\B3991AB_SQL.txt**
Output Set: **N:\CRF3\10292001\I840243A.raw**

<110> APPLICANT: NOVIMMUNE SA

<120> TITLE OF INVENTION: NEW TRANSCRIPTION FACTOR OF MHC CLASS II GENES, SUBSTANCES CAPABLE OF INHIBITING THIS NEW TRANSCRIPTION FACTOR AND MEDICAL USES OF THESE SUBSTANCES

<130> FILE REFERENCE: B3991AB-CS/KR

<140> CURRENT APPLICATION NUMBER: US/09/840,243A

<141> CURRENT FILING DATE: 2001-04-24

<150> PRIOR APPLICATION NUMBER: 98120085.0

<151> PRIOR FILING DATE: 1998-10-24

<160> NUMBER OF SEQ ID NOS: 19

<170> SOFTWARE: PatentIn Ver. 2.1

<210> SEQ ID NO: 1
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:primer
<400> SEQUENCE: 1
ccgtacgcgt ctagaccatg gagcttaccc agcctgcaga 40

<210> SEQ ID NO: 2
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:primer
<400> SEQUENCE: 2
ttcgaattct cgagtgtctg agtccccggc a 31

<210> SEQ ID NO: 3
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:primer
<400> SEQUENCE: 3
ccgtacgcgt ctagaccatg gagcccactc aggttgc 37

<210> SEQ ID NO: 4
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:primer
<400> SEQUENCE: 4
ttcgaattct cgagtgcctg ggttccagca gg 32

Errored check digit

<210> SEQ ID NO: 5
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING DATE: 10/29/2001
PATENT APPLICATION: US/09/840,243A TIME: 13:29:31

Input Set : A:\B3991AB_SQL.txt
Output Set: N:\CRF3\10292001\I840243A.raw

74 <220> FEATURE:
75 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
77 <400> SEQUENCE: 5
78 ccagctctag actccaccac tctcaccaac 30
81 <210> SEQ ID NO: 6
82 <211> LENGTH: 30
83 <212> TYPE: DNA
84 <213> ORGANISM: Artificial Sequence
86 <220> FEATURE:
87 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
89 <400> SEQUENCE: 6
90 ccttcgaatt ctcgctcttt tgccaggatg 30
93 <210> SEQ ID NO: 7
94 <211> LENGTH: 30
95 <212> TYPE: DNA
96 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
101 <400> SEQUENCE: 7
102 ggttctctag attggcagca ctggggatag 30
105 <210> SEQ ID NO: 8
106 <211> LENGTH: 30
107 <212> TYPE: DNA
108 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE:
111 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
113 <400> SEQUENCE: 8
114 gctacgaatt ccagcagaca cagccaaaac 30
117 <210> SEQ ID NO: 9
118 <211> LENGTH: 69
119 <212> TYPE: DNA
120 <213> ORGANISM: Artificial Sequence
122 <220> FEATURE:
123 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
125 <400> SEQUENCE: 9
126 ccgtacgcgt ctagaatgga ttacaaagac gatgacgata agatggagct tacccagcct 60
128 gcagaagac 69
131 <210> SEQ ID NO: 10
132 <211> LENGTH: 1345
133 <212> TYPE: DNA
134 <213> ORGANISM: Homo sapiens
136 <220> FEATURE:
137 <221> NAME/KEY: CDS
138 <222> LOCATION: (418)..(1200)
140 <400> SEQUENCE: 10
141 acgcagggaa ggaggcacac ccgggggtgg cgcagtgagg agggggcgcg acggccagga 60
143 ggctggtgga gcgacaccca ggcaggagag ggggaagaac tctctccctt tctgaacccc 120
145 cttttccttg agagacgagt tgggggagtc ctccacgcat tacccactcg ggccgcaaaa 180
147 actcccttct ttagccctct gccccccgccc ttgcttataa gcctttgaga ccgcagaagg 240

RAW SEQUENCE LISTING DATE: 10/29/2001
PATENT APPLICATION: **US/09/840,243A** TIME: 13:29:31

Input Set : **A:\B3991AB_SQL.txt**
Output Set: **N:\CRF3\10292001\I840243A.raw**

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149 gaccttgttg tggaacggga cggccaagag gaagccagat cgctgagggt ccggtctcca 300
151 gtttgcctcc tgctatatcc attggaagag aaaagtttgt gacttgggcc cccaagtttt 360
153 gagagaactg ggctttcggc gcgggggggac agaggaggct cgtggggagc tttcccc    417
155 atg gag ctt acc cag cct gca gaa gac ctc atc cag acc cag cag acc    465
156 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
157   1               5                  10                  15
159 cct gcc tca gaa ctt ggg gac cct gaa gac ccc gga gag gag gct gca    513
160 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
161             20                  25                  30
163 gat ggc tca gac act gtg gtc ctc agt ctc ttt ccc tgc acc cct gag    561
164 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
165         35                  40                  45
167 cct gtg aat cct gaa ccg gat gcc agt gtt tcc tct cca cag gca ggc    609
168 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
169     50                  55                  60
171 agc tcc ctg aag cac tcc acc act ctc acc aac cgg cag cga ggg aac    657
172 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
173  65                  70                  75                  80
175 gag gtg tca gct ctg ccg gcc acc cta gac tcc ctg tcc atc cac cag    705
176 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
177                 85                  90                  95
179 ctc gca gca cag ggg gag ctg gac cag ctg aag gag cat ttg cgg aaa    753
180 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
181             100                 105                 110
183 ggt gac aac ctc gtc aac aag cca gac gag cgc ggc ttc acc ccc ctc    801
184 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
185         115                 120                 125
187 atc tgg gcc tcc gcc ttt gga gag att gag acc gtt cgc ttc ctg ctg    849
188 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
189     130                 135                 140
191 gag tgg ggt gcc gac ccc cac atc ctg gca aaa gag cga gag agc gcc    897
192 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
193 145                 150                 155                 160
195 ctg tcg ctg gcc agc aca ggc ggc tac aca gac att gtg ggg ctg ctg    945
196 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
197                 165                 170                 175
199 ctg gag cgt gac gtg gac atc aac atc tat gat tgg aat gga ggg acg    993
200 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
201             180                 185                 190
203 cca ctg ctg tac gct gtg cgc ggg aac cac gtg aaa tgc gtt gag gcc   1041
204 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
205         195                 200                 205
207 ttg ctg gcc cga ggc gct gac ctc acc acc gaa gcc gac tct ggc tac   1089
208 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
209     210                 215                 220
211 acc ccg atg gac ctt gcc gtg gcc ctg gga tac cgg aaa gtg caa cag   1137
212 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
213 225                 230                 235                 240
215 gtg atc gag aac cac atc ctc aag ctc ttc cag agc aac ctg gtg ccc   1185
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RAW SEQUENCE LISTING DATE: 10/29/2001
PATENT APPLICATION: **US/09/840,243A** TIME: 13:29:31

Input Set : **A:\B3991AB_SQL.txt**
Output Set: **N:\CRF3\10292001\I840243A.raw**

```
216 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
217                 245                 250                 255
219 gct gac cct gag tga aggccgcctg ccggggactc agacactcag ggaacaaaat   1240
220 Ala Asp Pro Glu
221             260
223 ggtcagccag agctggggaa acccagaact gacttcaaag gcagcttctg gacaggtggt 1300
225 gggaggggac ccttcccaag aggaaccaat aaaccttctg tgcag                1345
228 <210> SEQ ID NO: 11
229 <211> LENGTH: 260
230 <212> TYPE: PRT
231 <213> ORGANISM: Homo sapiens
233 <400> SEQUENCE: 11
234 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
235   1               5                  10                  15
237 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
238             20                  25                  30
240 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
241         35                  40                  45
243 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
244     50                  55                  60
246 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
247 65                  70                  75                  80
249 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
250                 85                  90                  95
252 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
253             100                 105                 110
255 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
256         115                 120                 125
258 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
259     130                 135                 140
261 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
262 145                 150                 155                 160
264 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
265                 165                 170                 175
267 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
268             180                 185                 190
270 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
271         195                 200                 205
273 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
274     210                 215                 220
276 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
277 225                 230                 235                 240
279 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
280                 245                 250                 255
282 Ala Asp Pro Glu
283             260
292 <210> SEQ ID NO: 12
293 <211> LENGTH: 260
294 <212> TYPE: PRT
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RAW SEQUENCE LISTING DATE: 10/29/2001
PATENT APPLICATION: **US/09/840,243A** TIME: 13:29:31

Input Set : **A:\B3991AB_SQL.txt**
Output Set: **N:\CRF3\10292001\I840243A.raw**

295 <213> ORGANISM: Homo sapiens
297 <400> SEQUENCE: 12
298 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
299 1 5 10 15
301 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
302 20 25 30
304 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
305 35 40 45
307 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
308 50 55 60
310 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
311 65 70 75 80
313 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
314 85 90 95
316 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
317 100 105 110
319 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
320 115 120 125
322 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
323 130 135 140
325 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
326 145 150 155 160
328 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
329 165 170 175
331 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
332 180 185 190
334 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
335 195 200 205
337 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
338 210 215 220
340 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
341 225 230 235 240
343 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
344 245 250 255
346 Ala Asp Pro Glu
347 260
350 <210> SEQ ID NO: 13
351 <211> LENGTH: 269
352 <212> TYPE: PRT
353 <213> ORGANISM: Murinae gen. sp.
355 <400> SEQUENCE: 13
356 Met Glu Pro Thr Gln Val Ala Glu Asn Leu Val Pro Asn Gln Gln Pro
357 1 5 10 15
359 Pro Val Pro Asp Leu Glu Asp Pro Glu Asp Thr Arg Asp Glu Ser Pro
360 20 25 30
362 Glu Asn Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Asp
363 35 40 45
365 Ala Val Asn Pro Glu Ala Asp Ala Ser Ala Ser Ser Leu Gln Gly Ser
366 50 55 60

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

<210> SEQ ID NO 18
<211> LENGTH: 220
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: UNSURE
<222> LOCATION: 31
<221> NAME/KEY: UNSURE
<222> LOCATION: 148
<221> NAME/KEY: UNSURE
<222> LOCATION: 159
<400> SEQUENCE: 18

12:30 pm 11/07/01

Sequence listing as of the above time and date.

Field 223 is required to enumerate unknown Xaa and possible values

VERIFICATION SUMMARY DATE: 10/29/2001
PATENT APPLICATION: **US/09/840,243A** TIME: 13:29:32

Input Set : **A:\B3991AB_SQL.txt**
Output Set: **N:\CRF3\10292001\I840243A.raw**

L:496 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18
L:496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:520 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18
L:520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18